# Claims

What is claimed:

[c1]

1.A method to eliminate redundant sequences which are common between two or more samples using bimolecular degrading enzymatic reagents and radiolabeled assay to identify the remaining sequences which are uniquely expressed or over and under expressed in these samples, comprising of the steps:

a). isolating RNAs or DNAs from samples which are of interest,

b). generating cDNA from RNAs using RT-PCR methods and technologies,

c). cross mixing complementary cDNAs with RNAs of samples of interest,

d). degrading the hybridized complements using degrading reagents,

e). amplifying resultant cDNAs or RNAs by PCR amplification,

f). displaying and reading resultant cDNAs or RNAs, and

h). sequencing unique cDNAs or RNAs.

[c2]

2.The method of claim 1, wherein said samples of interest recited in (a) are cells, tissues, pathogens, plants, and animals which RNAs and DNAs are isolated using standard prior art methods and technologies.

[c3]

3.The samples of claim 2, are comprised of cells, tissues, pathogens, plants, and animals with little or totally known genetic sequence information.

[c4]

4.The samples of claim 2 are comprised of cells, tissues, pathogens, plants, and animals, which have differentiated due to a diseased state, developmental, change, or induced by an external or internal stimulus.

[c5]

5.The method of claim 1, wherein said RT-PCR methods and technologies is comprised of radioactive labeled to anchored oligo dT primers to generating cDNAs or RNAs.

[c6]

6.The method of claim 1, wherein said cross mixing complementary samples comprise of mixing cDNAs and RNAs from samples recited in Claims 3 and 4 forming hybridized cDNA/RNA.

[c7]

7.The method of claim 1, wherein said degrading reagents recited in d) are Exonuclease III or VII enzyme.

[c8]

8.The method of claim 1, wherein said amplifying by PCR recited in e) comprises of using AmpliTaq Gold Polymerase.

[c9]

9.The method of claim 1, wherein said displaying resultant cDNAs or RNAs recited in f) is a electrophoresis gel or capillary electrophoresis.

[c10]

10.The method of claim 1, wherein said reading resultant cDNAs or RNAs recited in f) is a photographic plate.

[c11]

11.The method of claim 1, wherein said sequencing cDNAs or RNAs recited in h) is performed by a MegaBace DNA sequencer or similar automated sequencers.

[c12]

12.A method to eliminate redundant sequences which are common between two or more samples using bimolecular degrading enzymatic reagents and fluorescence dye assay to identify the remaining sequences which are uniquely expressed or over and under expressed in these samples, comprising of the steps;

a). isolating of RNAs or DNAs from samples which are of interest,

b). generating cDNA from RNAs using RT-PCR methods and technologies,

c). cross mixing complementary cDNAs with RNAs of samples of interest,

d). degrading the hybridized complements using degrading reagents,

e). amplifying resultant cDNAs or RNAs by PCR amplification,

f). displaying and reading resultant cDNAs or RNAs, and

h). sequencing unique cDNAs or RNAs.

[c13]

13.The method of claim 12, wherein said samples of interest recited in (a) are cells, tissues, pathogens, plants, and animals which RNAs and DNAs are isolated using standard prior art methods and technologies.

[c14]

14.The samples of claim 12, are comprised of cells, tissues, pathogens, plants, and animals with little or totally unknown genetic sequence information.

[c15]

15. The samples of claim 12 are comprised of cells, tissues, pathogens, plants, and animals, which have differentiated due to a diseased state, developmental, change, or induced by an external or internal stimulus.

[c16]

16.The method of claim 12, wherein said RT-PCR methods and technologies is comprised of fluorescence dyes labeled to anchored oligo dT primers to generate cDNAs or RNAs.

[c17]

17.The fluorescence dyes of claim 16, are dyes which absorb and fluorescence at two distinct wavelengths, are fluorescence quencher pairs, fluorescence a two distinct fluorescence lifetimes, and fluorescence at two distinct polarizations.

[c18]

18.The method of claim 12, wherein said cross mixing complementary samples comprise of mixing cDNAs and RNAs from samples recited in Claims 3 and 4 forming hybridized cDNA/RNA.

[c19]

19.The method of claim 12, wherein said degrading reagents recited in d) are Exonuclease III or VII enzyme.

[c20]

20.The method of claim 12, wherein said amplifying by PCR recited in e) comprises of using AmpliTaq Gold Polymerase.

[c21]

21.The method of claim 12, wherein said displaying resultant cDNAs or RNAs recited in f) is a electrophoresis gel or capillary electrophoresis.

[c22]

22.The method of claim 12, wherein said reading resultant cDNAs or RNAs recited in f) is a scanning fluorescence spectrophotometer.

[c23]

23.The method of claim 12, wherein said sequencing cDNAs or RNAs recited in h) is by a MegaBace DNA sequencer or similar automated sequencers.

[c24]

24.A method to degrading cDNA/RNA, or cDNA/cDNA or RNA/RNA hybrids using S1 nuclease enzyme to eliminate common cDNA's or RNA's from two different cell and tissue types.

[c25]

25.A method to degrading cDNA/RNA, or cDNA/cDNA or RNA/RNA hybrids using Exonuclease enzyme to eliminate common cDNA's or RNA's from two different cell and tissue types.